

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of Brian K. Haarer and Nigel S. Atkinson
Serial No.: Not yet assigned Group Art Unit:
Filed: Herewith Examiner:

For: **DNA ADDITIVES AS A MECHANISM FOR UNAMBIGUOUSLY MARKING
BIOLOGICAL SAMPLES**

Assistant Commissioner of Patents and Trademarks
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Washington, D.C. 20231

Dear Sir:

Enclosed please find the following:

1. Specification, abstract and claims (2 independent, 16 dependent, 18 total) (15 pages);
2. Informal drawings (3 figures, 3 sheets);
3. Declaration and Power of Attorney;
4. Verified Statement Claiming Small Entity Status - Independent Inventor;
5. Two checks totaling the amount of \$380.00; and,
6. Certificate of Express mailing.

The Commissioner is hereby authorized to charge any fee deficiency, or credit any overpayment, to Deposit Account No. 18-1579. The Commissioner is also authorized to charge Deposit Account No. 18-1579 for any future fees connected in any way to this application. Two copies of this letter are enclosed.

Respectfully submitted,

Thomas A. Corrado

Thomas A. Corrado, Esq.
Registration No. 42,439
Roberts & Abokhair, LLC
11800 Sunrise Valley Drive, Suite 1000
Reston, VA 20191
(703) 391-2900

02/22/99
jc630 U.S. PTO

jc542 U.S. PTO
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**VERIFIED STATEMENT CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(f) & 1.27(b))--INDEPENDENT INVENTOR**

Docket Number (Optional)

Applicant or Patentee: Brian K. Haarer and Nigel S. AtkinsonSerial or Patent No.: Not Yet IssuedFiled or Issued: HerewithTitle: DNA Additives As A Mechanism For Unambiguously Marking Biological Samples

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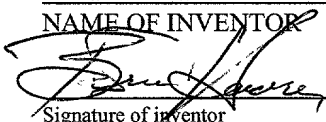
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I hereby declare that all statements made herein of my own knowledge are true and that all statements made an information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Brian K. Haarer

NAME OF INVENTOR



Signature of inventor

1-13-99

Date

NAME OF INVENTOR

Signature of inventor

Date

NAME OF INVENTOR

Signature of inventor

Date

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Nigel S. Atkinson
NAME OF INVENTOR


Signature of inventor

1/13/99
Date

NAME OF INVENTOR

Signature of inventor

Date

NAME OF INVENTOR

Signature of inventor

Date

DNA Additives as a Mechanism for Unambiguously Marking Biological Samples

Inventors: Brian K. Haarer and Nigel S. Atkinson

Field of the Invention

The present invention relates generally to the forensic or medical analysis of biological samples. More specifically, the present invention relates to the marking of biological samples for their subsequent distinction from unmarked biological samples in standard forensic nucleic acid analysis.

Background of the Invention

In certain criminal investigations, "known" biological samples (primarily blood, saliva, and semen) are collected from victims, suspects, and their relatives. In these criminal investigations, "unknown" biological specimens are also collected, generally from the crime scene and from residences, automobiles, and other items associated with one or more suspects in the investigation. These unknown biological specimens are often scrapings of drops of blood, saliva, semen, or small tissue fragments.

Both known and unknown biological specimens are subjected to various analyses, including characterizations of their constituent deoxyribonucleic acid (DNA). The standard analysis methods used are (a) analysis of *Variable Numbers of Tandem Repeats (VNTR)*, (b) analysis of *Short Tandem Repeats (STR)*, (c) analysis of Single Nucleotide Polymorphisms (SNP), (d) analysis of *Restriction Fragment Length Polymorphisms (RFLPs)*, and (e) analysis of mitochondrial DNA sequences. VNTR and STR analyses utilize simple or multiplex *Polymerase Chain Reaction (PCR)* technology; RFLP analysis utilizes restriction enzyme digestion of DNA followed by DNA hybridization techniques with labeled DNA probes; and mitochondrial DNA sequence analysis utilizes a combination of PCR technology and conventional dideoxy ("Sanger") sequencing in a process known as *cycle sequencing*.

Results from the above analyses are used to compare the known and unknown samples to determine any possible relationships between the samples.

However, problems may arise due to the deliberate or inadvertent contamination of

1 unknown biological samples by previously collected known biological samples, or by subsequent
2 samples due to the confusion of samples (e.g. during analysis). In the example of criminal
3 forensic analysis, such contamination could arise when blood from a victim is collected at a
4 particular location, then transported to the residence of a suspect and subsequently released at the
5 suspect's residence.

6 Thus a need exists for a mechanism whereby collected known biological samples would
7 be unambiguously marked and identified at the time of collection. Then, if a marked sample
8 should happen to contaminate another locale, the sample would be recognized as a contaminant
9 upon subsequent analysis. This would also safeguard against the confusion of samples during
10 analysis, preventing a "known" sample from being mistaken as a sample collected from a crime
11 scene.

12 **Summary of the Invention**

13 It is therefore an object of the present invention to prevent confusion of known forensic or
14 other biological samples with unknown samples, by adding a DNA molecule of defined
15 composition to the known sample at the time of sample collection.

16 It is a further object of the present invention to have the added DNA molecule be
17 detectable through standard methods of forensic analysis, without interfering with, or confusing
18 the results of, such methods of analysis.

19 It is a further object of the present invention to decrease, if not eliminate, the possibility
20 that collected biological samples could subsequently serve to contaminate some other person,
21 place, or thing without being detected as an obvious contaminant.

22 It is a further object of the present invention to provide confirmation that known and
23 unknown samples have not been confused during analysis, and to provide instant notification if
24 such confusion does take place.

25 It is a further object of the present invention to improve the integrity of the data, such that
26 analysis results are more likely to hold up in court.

27 It is a further object of the present invention to provide a marker for the known samples
28 that shows up during the course of forensic analysis, and therefore does not require special
29 detection methods beyond the inclusion of appropriate DNA primers or hybridization probes,

1 depending on the method of analysis.

2 The present invention accomplishes the above and other objectives by providing a
3 mechanism for marking biological samples (blood, semen, saliva, etc.) that are to be used for
4 subsequent nucleic acid analysis. The method involves adding a nucleic acid (DNA) molecule of
5 known sequence to the biological sample at the time of sample collection. The method further
6 utilizes primers specific to the complementary strands of the added DNA such that they will
7 direct the synthesis of another DNA molecule of known length when used in a standard or
8 multiplex polymerase chain reaction (PCR). This provides an unambiguous identifying label for
9 the collected forensic or medical samples, including blood, semen, saliva, urine, tissue, and
10 mixtures of bodily fluids. When used with the supplied primers or DNA probe(s), PCR or
11 nucleic acid hybridization techniques will produce or recognize DNA fragments of
12 predetermined size(s), preventing errant confusion of said samples with other forensic or medical
13 samples that do not contain the aforementioned DNA additive.

14 **Brief Description of the Drawings**

15 **Figure 1** illustrates the basic DNA additive and single primer set.

16 **Figures 2A-2C** illustrate alternative methods for generating two distinct fragments from PCR
17 reactions(s).

18 **Figure 2A** illustrates a single template used with two alternative sets of primers.

19 **Figure 2B** illustrates two templates used with a single set of primers.

20 **Figure 2C** illustrates two templates used with two alternative sets of primers.

21 **Figure 3** illustrates restriction sites at ends of DNA additive for use with RFLP analysis.

22 **Detailed Description of the Invention**

23 The present invention is a process whereby a defined and unique marker DNA is added to
24 biological samples collected from known individuals by standard methods. Such tagging of
25 collected samples effectively prevents their subsequent confusion with samples ("unknowns")
26 that do not contain the defined marker DNA. Examples of unknown biological samples would
27 be those collected at crime scenes or from crime victims, including but not limited to blood
28 scrapings, hair, semen, saliva, blood, tissue scrapings, urine, mixtures of body fluids, etc.

29 The present invention is consistent with commonly used techniques for forensic analysis.

1 These include Short Tandem Repeat (STR), Variable Number of Tandem Repeats (VNTR),
2 Single Nucleotide Polymorphisms (SNP), Restriction Fragment Length Polymorphism (RFLP),
3 and mitochondrial sequencing analysis methods. These techniques are well known to those
4 skilled in the art, and are described in the following references, each of which is incorporated
5 herein by reference in its entirety.

6 (i) General reference for RFLP, VNTR, STR, and mitochondrial sequencing (the second
7 reference also includes SNP, though not by that name):

8 Lincoln, P.J., and J. Thomson, eds. 1998. Forensic DNA Profiling Protocols. Humana
9 Press, Inc.

10 Landegren, U., R. Kaiser, C.T. Caskey, and L. Hood. 1988. DNA diagnostics—
11 molecular techniques and automation. Science. 242:229-237.

12 (ii) RFLP analysis:

13 Botstein, D., R.L. White, M. Skolnick, R.W. Davis. 1980. Construction of a genetic
14 linkage map in man using restriction fragment length polymorphisms. Am. J. Hum.
15 Genet. 32:314-331.

16 (iii) VNTR analysis:

17 Nakamura et al. 1987. Variable number of tandem repeat (VNTR) markers for human
18 gene mapping. Science. 235:1616-1622.

19 (iv) STR analysis:

20 Edwards, A., A. Civitello, H.A. Hammond, and C.T. Caskey. 1991. DNA typing and
21 genetic mapping with trimeric and tetrameric tandem repeats. Am. J. Hum. Genet.
22 49:746-756.

23 Ricciardone et al. 1997. Multiplex systems for the amplification of short tandem repeat
24 loci: evaluation of laser fluorescence detection. Biotechniques. 23:742-747.

25 (v) SNP analysis:

26 Nickerson, D.A., R. Kaiser, S. Lappin, J. Stewart, L. Hood, and U. Landegren. 1990.
27 Automated DNA diagnostics using an ELISA-based oligonucleotide ligation assay.
28 Proc. Natl. Acad. Sci. USA. 87:8923-8927.

29 Nikiforov, T.T., R.B. Rendle, P. Goelet, Y.H. Rogers, M.G. Kotewicz, S. Anderson, G.L.

1 Trainor, and M.R. Knapp. 1994. Genetic bit analysis: a solid phase method for
2 typing single nucleotide polymorphism. *Nucleic Acids Res.* 22:4167-4175.
3 Ross, P.L., K. Lee, and P. Belgrader. 1997. Discrimination of single-nucleotide
4 polymorphisms in human DNA using peptide nucleic acid probes detected by
5 MALDI-TOF mass spectrometry. *Anal. Chem.* 69:4197-4202.
6 (vi) General PCR analysis:
7 Mullis et al. 1986. Specific enzyme amplification of DNA in vitro: the polymerase chain
8 reaction. *Cold Spring Harbor Symp Quant. Biol.* 51:263-273.
9 Mullis, K.B., D.H. Gelfand, S. Stoffel, S.J. Scharf, R. Higuchi, G.T. Horn GT, K.B.
10 Mullis, and H.A. Erlich HA. 1988. Primer-directed enzymatic amplification on
11 DNA with thermostable DNA polymerase. *Science* 239:487-491.

12 In a preferred embodiment of the present invention, the DNA additive is introduced
13 irreversibly into the known samples at the time of collection. This can be accomplished by
14 providing the DNA additive in the most commonly used collection vessels, including vacutainer
15 tubes, FTA Blood Stain Collection Cards™ (or similar blood collection and preservation
16 systems), saliva collection swabs, etc.

17 The present invention comprises a fragment or fragments of DNA of known sequence
18 that are introduced into known samples. The DNA is provided either as an insert within a
19 plasmid host that allows amplification in *E. coli*, or is added as a linear fragment. The length of
20 the DNA(s) is such that it/they (a) provide PCR product(s) of known lengths when used with
21 appropriate oligonucleotide primers in a PCR reaction in conjunction with either STR or VNTR
22 analysis, (b) provide restriction fragments of known lengths that can be detected with defined
23 nucleic acid probes when used in RFLP analysis, and (c) generate a unique known DNA
24 sequence when used with the appropriate oligonucleotide sequencing primer(s) in conjunction
25 with mitochondrial sequencing (in cycle sequencing reactions).

26 Variations on the exact nature of the added DNA are shown in Figures 1-3. **Figure 1**
27 illustrates the basic form of the DNA additive, where the DNA fragment of known length and
28 sequence is used in conjunction with primers complementary to its two ends, such that a PCR
29 reaction utilizing these three components (DNA additive and two primers) will produce a PCR

1 product of defined length. This length should be of similar size to products generated by
2 standard STR or VNTR primer sets. The DNA additive consists of DNA fragment of known
3 sequence **102** inserted into a plasmid vector, (portions of the plasmid vector adjacent to the insert
4 are shown **104**). A single primer set consists of first PCR primer **106** and second PCR primer
5 **108** which are used to identify the presence of the DNA additive. In the PCR, first PCR primer
6 **106** and second PCR primer **108** amplify, from the DNA additive, a DNA fragment of known
7 size and sequence.

8 Since STR and VNTR analyses differ in the size range of PCR products generated, it may
9 be necessary to develop DNA additives that are capable of generating at least two sizes of PCR
10 products. This can be accomplished by one of the methods illustrated in Figures 2A-2C.

11 **Figure 2A** illustrates a single DNA additive that has binding sites for two different
12 primer sets; the primer set used is determined by the type of forensic analysis being performed.
13 First primer set is shown as first primer **202** and second primer **204**. Second primer set is shown
14 as third primer **206** and fourth primer **208**. A DNA fragment of known sequence **210** is inserted
15 into a plasmid vector, (portions of the plasmid vector adjacent to the insert are shown **212**). For
16 example, the first primer **202** and second primer **204** would be used in a PCR reaction with the
17 DNA additive to generate a DNA fragment of a size consistent with VNTR analysis, while the
18 third primer **206** and fourth primer **208** would be used in a separate PCR reaction with the DNA
19 additive to generate a DNA fragment of a size consistent with STR analysis, which examines
20 smaller DNA fragments than does VNTR analysis.

21 **Figure 2B** illustrates a means by which two distinct DNA additives could be provided
22 with a single primer set. Here, first DNA fragment of known sequence **214** is inserted into a
23 plasmid vector, (portions of the plasmid vector adjacent to the insert are shown **216**) and second
24 DNA fragment of known sequence **218** is inserted into a plasmid vector, (portions of the plasmid
25 vector adjacent to the insert are also shown **220**). The primer set consists of first primer **222** and
26 second primer **224**. In this situation, use of first primer **222** and second primer **224** in PCR
27 reactions simultaneously on the two DNA additives would generate DNA fragments consistent
28 with multiple methods of analysis. PCR from template **214** would generate a DNA fragment
29 consistent with methods such as VNTR, that analyze longer DNA fragments, and PCR from

1 template **218** would generate a DNA fragment consistent with methods such as STR, that analyze
2 shorter DNA fragments.

3 **Figure 2C** illustrates a means by which two distinct DNA additives could be provided
4 with two distinct primer sets. Here, two templates are used with two alternative sets of primers.
5 A first DNA fragment of known sequence **226** and a second DNA fragment of known sequence
6 **228** are each inserted into a plasmid vector, (portions of the plasmid vector adjacent to the first
7 insert **230** and the second insert **232** are shown). First primer set is shown as first primer **234** and
8 second primer **236**. Second primer set is shown as third primer **238** and fourth primer **240**.

9 The DNA additives in Figure 2A and 2C are compatible with DNA sequencing methods
10 as shown; the additive of Figure 2B is only compatible when an additional unique set of primers
11 specific for one of the two added DNA molecules is used for the DNA sequence analysis.

12 **Figure 3** illustrates the necessary features for use of the DNA additive in RFLP analysis;
13 this design can easily be incorporated into any of the additive methods described in Figures 2A-
14 2C. Known restriction enzyme site(s) are engineered at or near the ends of the DNA insert, and
15 are used to release a DNA fragment of known length and sequence from the DNA additive.
16 Enzyme one **302** and enzyme two **304** can represent the same or different restriction enzyme
17 recognition sequences, and can represent single or multiple known restriction enzyme recognition
18 sequences.

19 In a preferred embodiment, the DNA additive comprises one or more of the following
20 features:

- 21 (a) the added DNA is stable for a length of time comparable to the shelf life of collected
22 biological specimens;
- 23 (b) the added DNA and any primers used in conjunction with the added DNA do not interfere
24 with the chosen form of analysis, and do not produce any PCR products, restriction fragments,
25 bands detected by hybridization analysis, or DNA sequence other than expected for the added
26 DNA. This requirement holds for the effects of oligonucleotide primers specific to the added
27 DNA on DNA from the known biological sample, and for the effects of oligonucleotide primers
28 normally used in forensic analysis methods on the DNA additive.
- 29 (c) the added DNA is compatible with, and stable through, standard DNA preparation

1 procedures specific for the type of collection vessel and for the specific forensic analysis protocol
2 used;

3 (d) the concentration of the added DNA is such that it will be present in molar ratios similar
4 to those of analysis targets in the known biological sample after preparation of the sample for
5 analysis; and

6 (e) the DNA additive, or products generated from the DNA additive (e.g. by PCR), is
7 compatible with commonly used methodologies for the subsequent analysis of such products,
8 including, but not limited to: DNA hybridization analysis, agarose gel electrophoresis,
9 polyacrylamide gel electrophoresis, capillary electrophoresis, and matrix-assisted laser desorption
10 ionization time-of-flight (MALDI-TOF) mass spectrometry.

11 In practice, the present invention comprises adding a nucleic acid of known sequence to
12 standard collection vessels for forensic and medical biological samples; collecting the biological
13 samples in the collection vessel containing the known nucleic acid additive; extracting the DNA
14 from the biological sample; providing nucleic acid primers complementary to the known nucleic
15 acid additive and analyzing the extracted DNA using standard assay techniques in conjunction
16 with the provided primers. Standard assay techniques are known to those skilled in the art and
17 include but are not limited to PCR-based analysis of short tandem repeats; PCR-based analysis of
18 variable numbers of tandem repeats; DNA hybridization analysis of restriction fragment length
19 polymorphisms; and the sequencing of mitochondrial DNA. In alternative embodiments the
20 method can comprise: 1/ the use of a single primer set with a single DNA additive to produce a
21 PCR product of defined length; 2/ the use of multiple primer sets with a single DNA additive to
22 produce fragments of different sizes in separate PCR reactions, 3/ a single primer set used with
23 multiple DNA additives to produce multiple fragments in a PCR reaction, and/or 4/ multiple
24 primer sets used with multiple DNA additives to produce multiple fragments in a PCR reaction.

25 To support the process of the present invention, oligonucleotide primers or DNA
26 hybridization probes necessary for the appropriate detection of the added DNA could be supplied
27 either independently or as components of commonly used assay kits.

28 In practice, it is preferred that oligonucleotide primers or DNA hybridization probes used
29 for the detection of the DNA additive are used on all samples analyzed, regardless of whether

1 they contain the DNA additive. Therefore, it is advantageous to supply necessary primers as
2 standard components in STR and VNTR PCR reactions, Further, it is preferred that (cycle)
3 sequencing using primers specific for the DNA additive be performed on all samples being
4 analyzed for mitochondrial DNA sequence. Finally, it is preferred that DNA hybridization
5 probes specific for the DNA additive be used to probe all samples being tested by RFLP analysis.

6 Any given set of PCR primers might support amplification of a DNA fragment from the
7 genomes of a small percentage of the population that had not been identified during the design
8 and testing of the DNA additive. This could give rise to false positives. In practice, this does not
9 present much of a problem since the spuriously amplified fragment will most likely be a different
10 size than a fragment amplified from the DNA additive. Furthermore, DNA sequence analysis
11 could be used to confirm that the fragment arose as a result of amplification from the DNA
12 additive.

13 In a preferred embodiment, the additive will be designed so that it contains binding sites
14 for more than two PCR primers, thereby providing a simpler method to prevent the production of
15 false positives. In this case, the presence of the DNA additive can be confirmed by performing
16 multiple PCR reactions, each using a different set of primers. Each PCR reaction would generate
17 an amplification product of known size and sequence from the DNA additive. Samples that
18 contain the DNA additive would produce positive PCR reactions with all of the primer sets. The
19 ability to confirm the presence of the additive by multiplex PCR greatly increases the robustness
20 of the procedure.

21 In an alternative embodiment, different DNA additives are used for different individuals
22 to provide further protection against mislabeling the samples. Here, if the DNA additive which
23 was to have been used for Jane Doe is found in the sample labeled John Smith, then additional
24 sampling of the possibly misidentified individuals would be indicated.

25 Having thus described the basic concept of the invention, it will be readily apparent to
26 those skilled in the art that the foregoing detailed disclosure is intended to be presented by way of
27 example only, and is not limiting. Various alterations, improvements and modifications will
28 occur and are intended to those skilled in the art, but are not expressly stated herein. These
29 modifications, alterations and improvements are intended to be suggested hereby, and within the

1 What is Claimed is:

2 1. A process for marking biological samples used in subsequent nucleic acid analysis
3 comprising:

4 collecting known biological samples;
5 introducing at least one fragment of deoxyribonucleic acid (DNA) of known length and
6 sequence into the known biological samples.

7 2. The process for marking biological samples used in subsequent nucleic acid
8 analysis of claim 1, where introducing at least one fragment of DNA further comprises:
9 providing the DNA fragment as an insert within a plasmid host that allows amplification
10 in *E. coli*.

11 3. The process for marking biological samples used in subsequent nucleic acid
12 analysis of claim 1, where introducing at least one fragment of DNA further comprises:
13 providing the DNA fragment as a linear fragment.

14 4. The process for marking biological samples used in subsequent nucleic acid
15 analysis of claim 1, where introducing at least one fragment of DNA further comprises:
16 inserting the DNA fragment into a plasmid vector.

17 5. The process for marking biological samples used in subsequent nucleic acid
18 analysis of claim 4, further comprising:
19 identifying the DNA fragment through the presence of a first polymerase chain reaction
20 primer and a second polymerase chain reaction primer.

21 6. The process for marking biological samples used in subsequent nucleic acid
22 analysis of claim 1, where the known length of the DNA fragment complies with a protocol and
23 where the protocol is selected from the group of protocols consisting of (1) a length of DNA
24 which provides PCR product(s) of known lengths when used with appropriate oligonucleotide
25 primers as known in the art, in a PCR reaction in conjunction with short tandem repeats analysis,
26 (2) a length of DNA which provides PCR product(s) of known lengths when used with
27 appropriate oligonucleotide primers as known in the art, in a PCR reaction in conjunction with
28 variable numbers of tandem repeats analysis, (3) a length of DNA which can be detected with
29 defined nucleic acid probes when used in restriction fragment length polymorphisms, and (4) a

length of DNA which generates a unique known DNA sequence when used with the appropriate oligonucleotide sequencing primer(s) as known in the art with mitochondrial sequencing.

7. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 further comprising:

administering to the DNA fragment primers complementary to its two ends.

8. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 where the DNA fragment has binding sites for two different primers.

9. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 where a first DNA fragment is inserted into a first plasmid vector and a second DNA fragment is inserted into a second plasmid vector.

10. The process for marking biological samples used in subsequent nucleic acid analysis of claim 9, where the first DNA fragment and the second DNA fragment each have binding sites for two different primers.

11. The process for marking biological samples used in subsequent nucleic acid analysis of claim 6, where the DNA fragment has at least one attribute selected from the list of attributes consisting of (1) the DNA fragment has a stability comparable to the shelf life of biological specimens, (2) the DNA fragment in conjunction with primers used in the addition thereof does not interfere with the subsequent analysis of the known biological sample, (3) the DNA fragment in conjunction with primers used in the addition thereof does not produce any polymerase chain reaction products, restriction fragments, bands detected by hybridization analysis, or DNA sequence other than expected for the added DNA fragment, (4) the DNA fragment is compatible with, and stable through, standard DNA preparation procedures as known in the art, (5) the concentration of the DNA fragment is of a predetermined amount such that it will be present in molar ratios similar to those of the analysis targets in the known biological samples after preparation of the sample for analysis and (6) the DNA fragment, or products generated from the DNA fragment, is compatible with at least one of DNA hybridization analysis, agarose gel electrophoresis, polyacrylamide gel electrophoresis, capillary electrophoresis, or matrix assisted laser desorption ionization time-of-flight mass spectrometry.

12. The process for marking biological samples used in subsequent nucleic acid

analysis of claim 11, where the DNA fragment is added to a collection vessel.

13. A process for marking biological samples used in subsequent nucleic acid analysis comprising:

introducing at least one fragment of deoxyribonucleic acid (DNA) of known length and sequence into a collection vessel;

collecting known biological samples;

adding the known biological samples to the collection vessel to obtain a modified biological sample;

extracting the DNA from the modified sample to obtain extracted DNA;

providing primers complementary to the extracted DNA to obtain a resulting sample;

analyzing the resulting sample using an assay technique selected from the list of assay techniques consisting of polymerase chain reaction-based analysis of short tandem repeats; polymerase chain reaction-based analysis of variable numbers of tandem repeats; DNA hybridization analysis of restriction fragment length polymorphisms; and the sequencing of mitochondrial DNA.

14. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing a polymerase chain reaction product of defined length using a single primer set with a single fragment of DNA.

15. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing fragments of differing sizes in separate polymerase chain reactions using multiple primer sets with a single fragment of DNA.

16. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

producing multiple fragments in a polymerase chain reaction using a single primer set with multiple DNA fragments.

17. The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, further comprising:

1 producing multiple fragments in a polymerase chain reaction using multiple primer sets
2 with multiple DNA fragments.

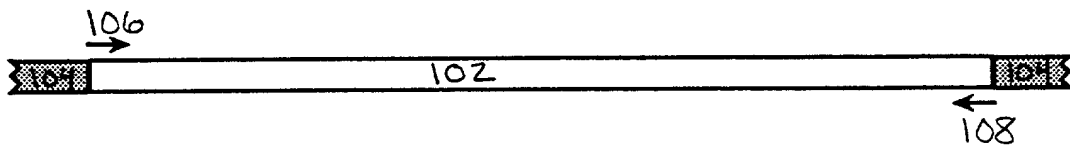
3 18. The process for marking biological samples used in subsequent nucleic acid
4 analysis of claim 13, where the primers are supplied as components of assay kits.

Case 2:09-cv-00000-01

Abstract

The present invention is directed to a mechanism for marking biological samples (blood, semen, saliva, etc.) that are to be used for subsequent nucleic acid analysis. The method involves adding a nucleic acid (DNA) molecule of known sequence to the biological sample at the time of sample collection. The method further utilizes primers specific to the complementary strands of the added DNA, such that they will direct the synthesis of another DNA molecule of known length when used in a standard or multiplex polymerase chain reaction (PCR). This provides an unambiguous identifying label for the collected forensic or medical samples, including blood, semen, saliva, urine, tissue, and mixtures of bodily fluids. When used with the supplied primers or DNA probe(s), PCR or nucleic acid hybridization techniques will produce or recognize DNA fragments of predetermined size(s), preventing errant confusion of said samples with other forensic or medical samples that do not contain the aforementioned DNA additive.

Figure 1



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Figure 2

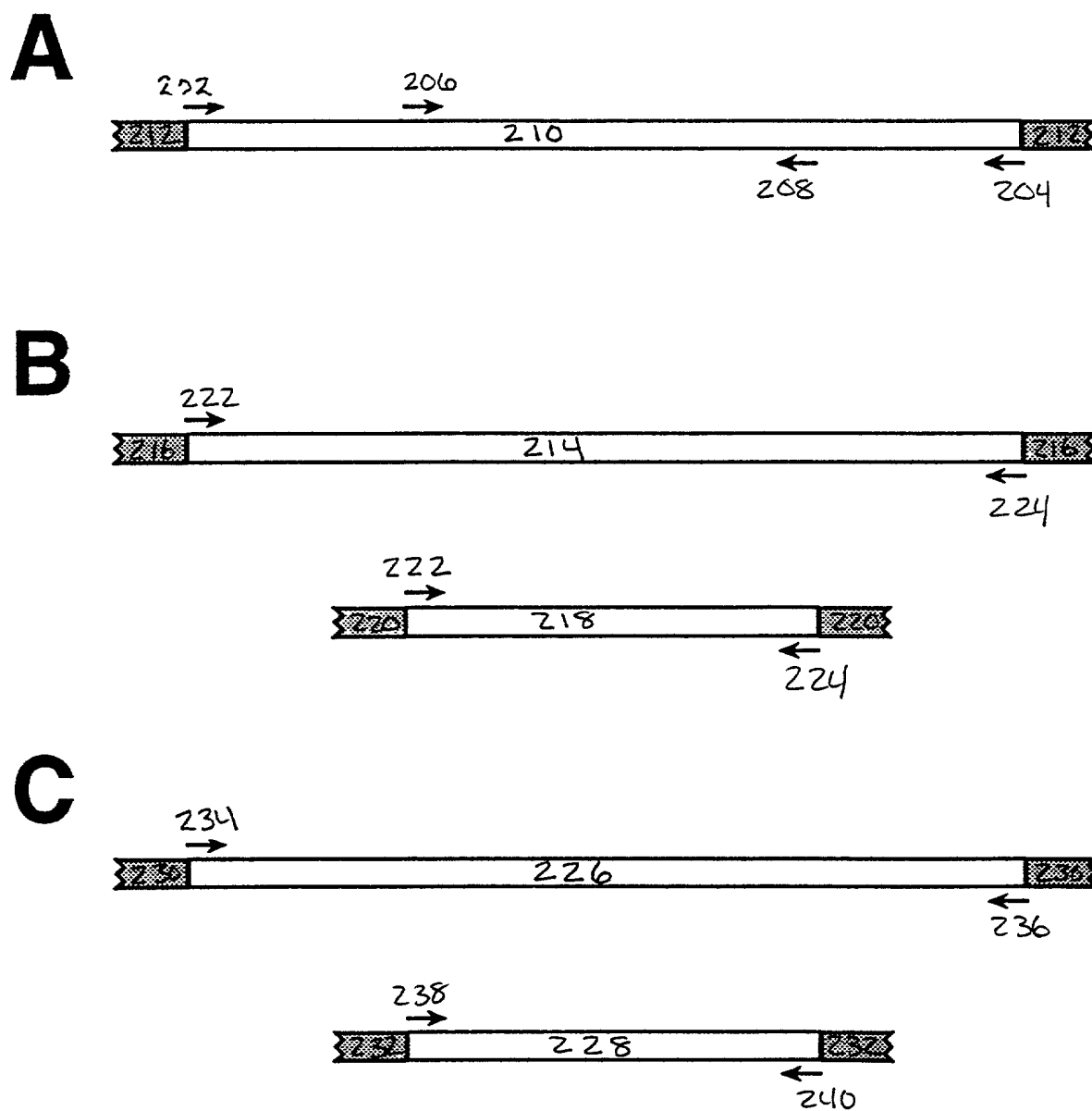


Figure 3



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of Brian K. Haarer and Nigel S. Atkinson

Serial No.: Not yet assigned Group Art Unit:

Filed: Herewith Examiner:

For: **DNA ADDITIVES AS A MECHANISM FOR UNAMBIGUOUSLY MARKING
BIOLOGICAL SAMPLES**

DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As below inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, joint and first inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled **DNA ADDITIVES AS A MECHANISM FOR UNAMBIGUOUSLY MARKING BIOLOGICAL SAMPLES**, the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, § 1.56(a).

I hereby appoint the following attorney(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

Jon L. Roberts
Registration No. 31,293
John K. Abokhair, Esq.
Registration No. 30,537
Thomas A. Corrado
Registration No. 42,439
Roberts & Abokhair, L.L.C.
11800 Sunrise Valley Drive
Suite 1000
Reston, Virginia 20191
(703) 391-2900

552220" 8346260

I declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of inventor Brian K. Haarer

Inventor's Signature  Date 1-13-99

Residence Austin, Texas

Post Office Address: 8008 Greenslope Drive
Austin, TX 78759

Citizenship: U.S.A.

652220"8345250

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11800 Sunrise Valley Drive
Suite 1000
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(703) 391-2900

552220" 3345260

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Full name of inventor Nigel S. Atkinson

Inventor's Signature *Nigel S. Atkinson* Date 1/13/99

Residence Round Rock, Texas

Post Office Address: 500 Peterson Street
Round Rock, TX 78759

Citizenship: U.S.A.

66240"8343250